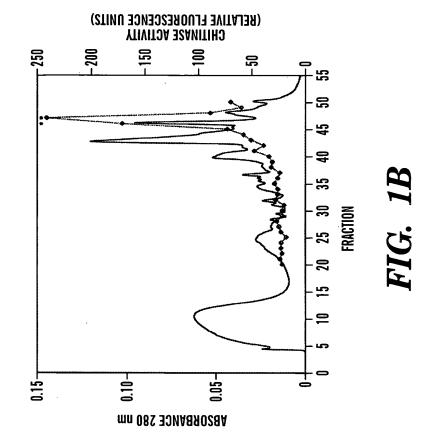
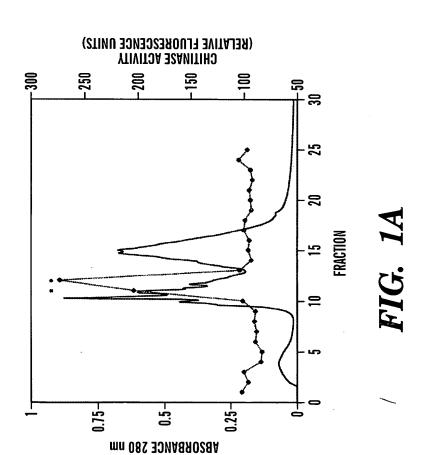


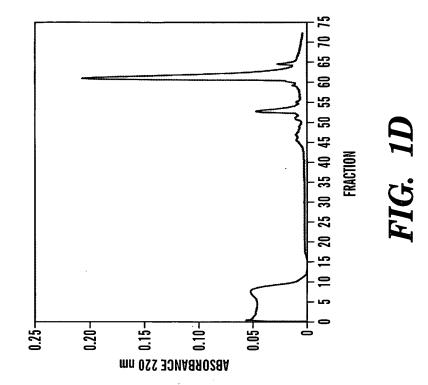
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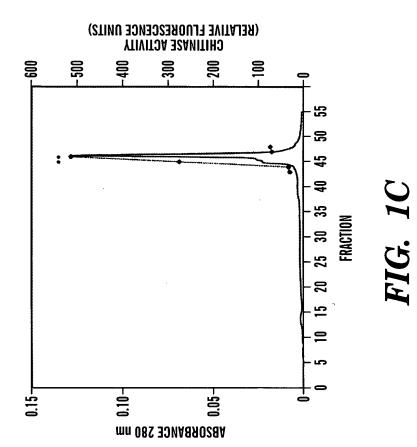






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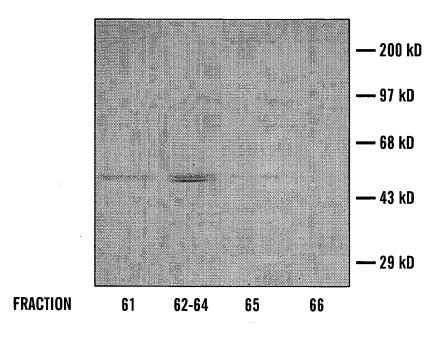


FIG. 1E

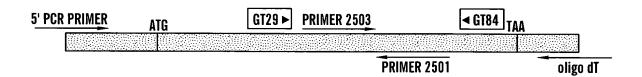


FIG. 2



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| WILK 1916 11 49 16 19 40 9K PER GRUNA LANGE GILLEGRENEN HALLE LHE                             | 20  |
|---|-----|
| N-terminal 1 N-terminal 2   |     |
| SFSHLKSNNSNFVETYGSYCGDGCNSTRITKNNKNINKNDRKSPRQILEEYK  | 100 |
| KRKQGIIAGYYGSWNSQGDRAKHMIDSNPMVSILYIAFARINMLYDVSRP  | 150 |
| Substrate binding site FNGRQRFLLRKHGLEYETYGMMLNEIRRIRKVRPDVIIL SLGGETYMID Active site peptide | 200 |
| I EKE I DYVDK I LKL VND DLDGVO I DWEPHGKFYNLNELNFSNYY I KL I N  Catalytic active site         | 250 |
| LLRKTIPEEKLISISGSSNAALSCVSGVASFCKDEESPYNTKFLSEQIET  | 300 |
| NKELHRAAAMLSAGTFINIFNTAKEKIDLVFIQTYNLETTNPDIMVDMYL  | 350 |
| SHLYFGLKYNITIILGFSLEHNRGGFSPENKELLELVGKTIHDKNQNNNR  | 400 |
| ADGIGIWHLFMKEQLPTGSFDVDIFLTNIWKHLNPEVQTPKDLTITENPE<br>GT33                                    | 450 |
| DCSTIDEYVPGLVIPTIGIYYKHNDAIWKTRSYSIHAPGVDRYEWDLVKV  | 500 |
| CYEKICDGKAAHYYNTDYKESSIIIWKGEPYLIKWWQQGPPEGQALESYT  | 550 |
| KLDASKCPGIEEWNKK <u>YPHKPLEVEEQY</u> EQEVDLPLQ*   | 587 |

FIG. 3





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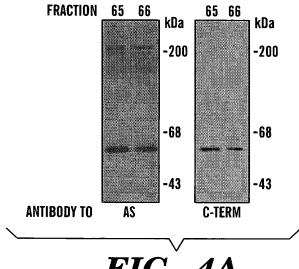


FIG. 4A

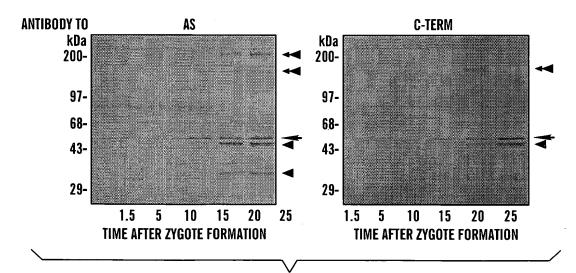


FIG. 4B

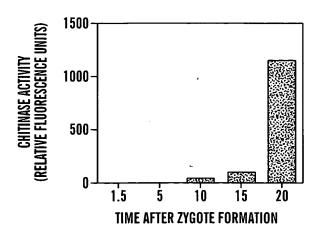
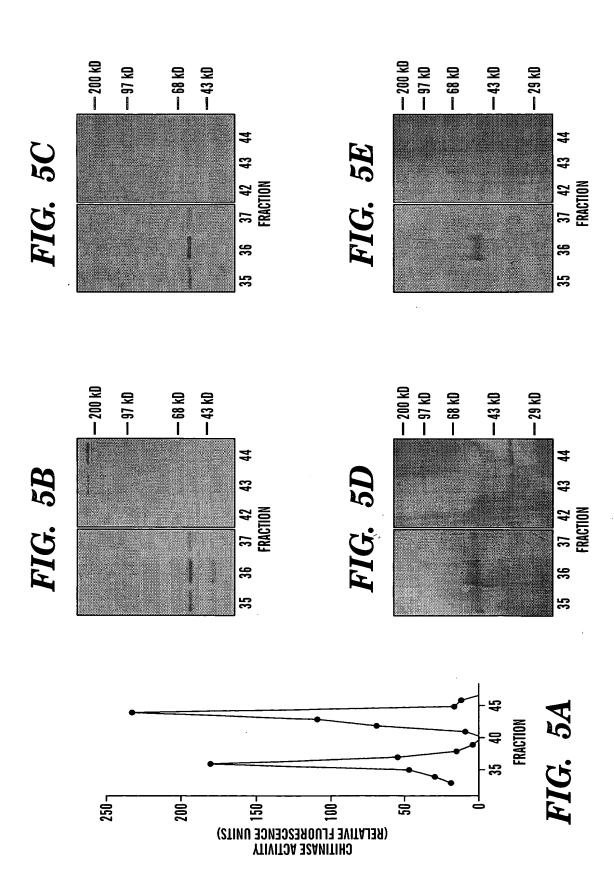
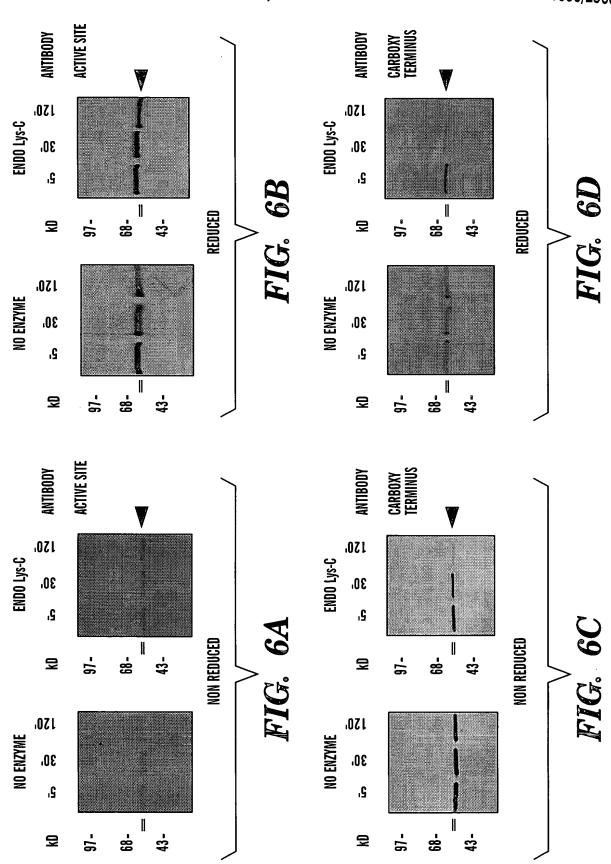


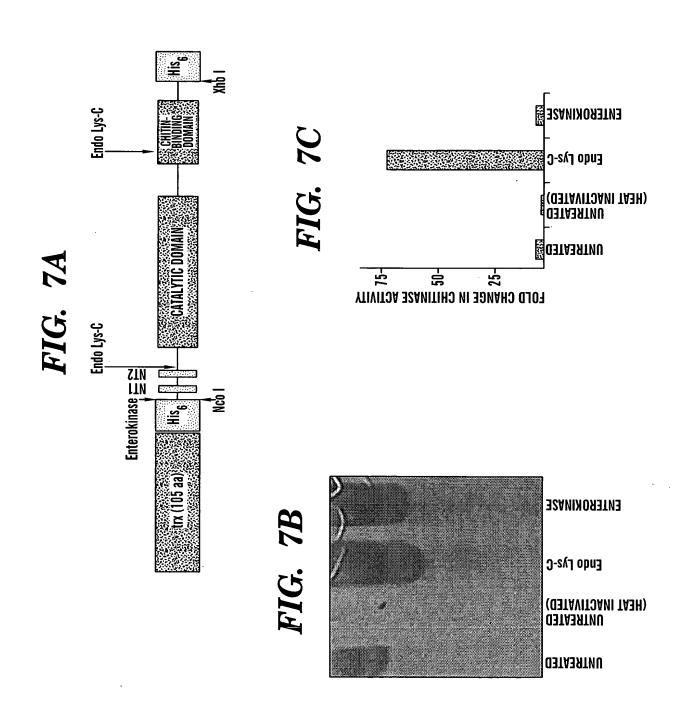
FIG. 4C



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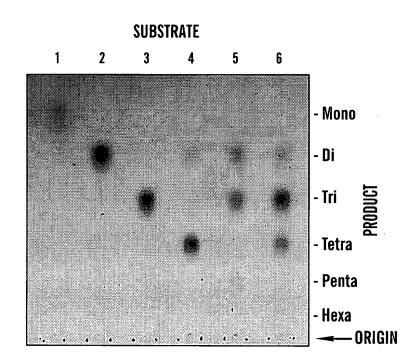
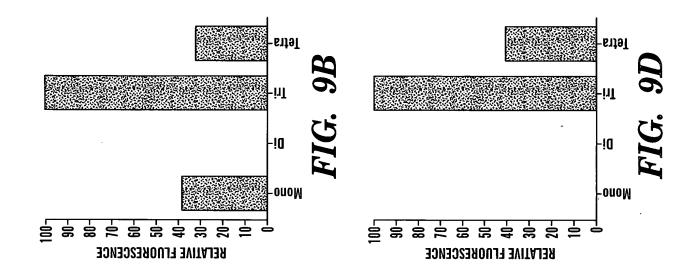


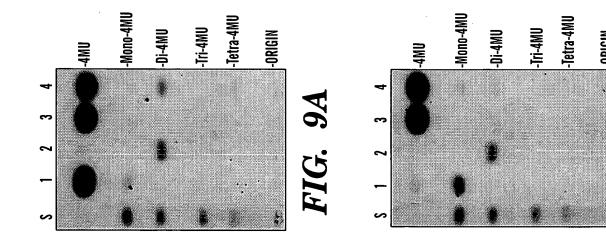
FIG. 8



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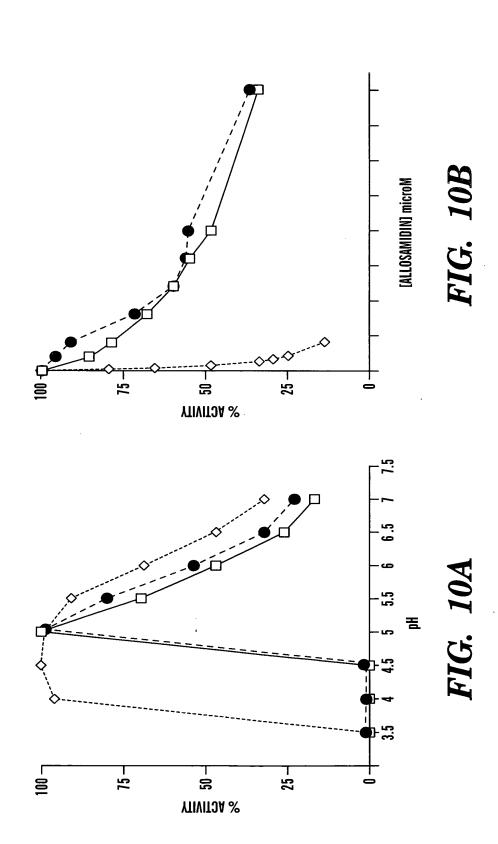






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| PfCHT1           | MNPTVKYSPLVICILISTYVSVIRG  |
|------------------|--|
| PgCHT1           | Pro-enzy me domain PRIFIT STRICT SANSRI LKGKNNINNSLGIIRENKNKTHOTEIHESPSHLKSNNSNEVE 64  |
| PfCHT1           | Catalytic domain begins HRARPGESR  |
| PgCHT1           | **: : *: . * . * . * :   |
| PfCHT1           | NT1 Substrate-binding site NPNLAVVHMSPAKADLSYDSIBSIVGSPLLPKSLIGLEYIGLNEYPNDAMNLRKARPDIIMILSIAGR 140                                |
| PgCHT1           |  |
| PfCHT1           |  |
| PgCHI            | TYM-IDIBKBIDYVDKILKLVNDPDLDGVDIDWEPHGKFYNLNBLNPSNYYIKLINLLKKTIPBBKLISI 264   |
| PfCHT1           | SQSSNGALSCI-GPNDPKKICMDDBAPYNSKYPNKP-DVKKBLLRAAQMASAGGAIYLANNLLOMIDMVF 278   |
| PgCHT1           | SGSSNAALSCVSGVASPCKDBBSPYNTKPLSBQIBTNKBLHRAAAMLSAGTFINIFNTAKBKIDLVF 331  |
| PfCHT1           | VQTPNYTNSTDSTVMKELYDSYAYYGKKYDYVIIMGPTLMPPSTPPNPNDKMLVKSIGDFVKTENKLNKR 348   |
| PgCHT1           | IQTYNL-ETTNPDIHVDAYLSHLYPGLKYNITIILGFSLEHNRGGPSPENKELLELVGKTIHDKNQNNNR 400   |
| PfCHT1           | Catalytic domain ends ADGFGLWSLSSDWAHNBQLAIEYFVBSLH. 378 Chitin-binding domain   |
| PgCHT1           | mailnpevotpkoltitenped   |
| PgCHT1<br>PgCHT1 | DYYKHAIWKTRSYSIHAPGVDRYBWDLVKVCYBKICDGKAAHYYNTDYKBSSIIIWKGBPYLIKWWQQGP 540<br>PBGQALBSYTKLDASKCPGIBBWNKKYPHKPLEVBBQYBQBVDLPLQ. 587 |



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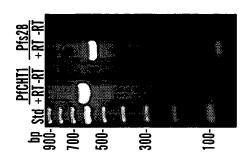
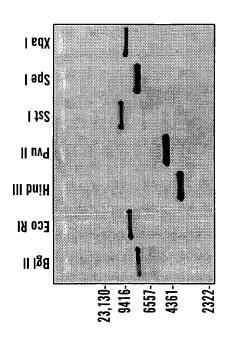


FIG. 12C

FIG. 12B

FIG. 12A





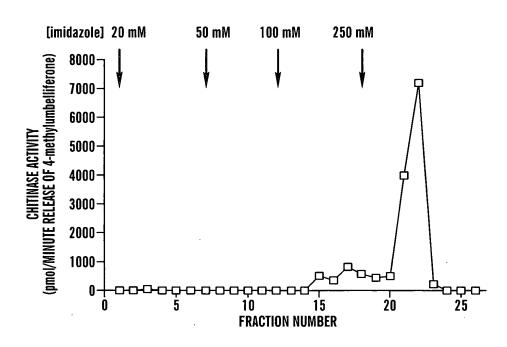
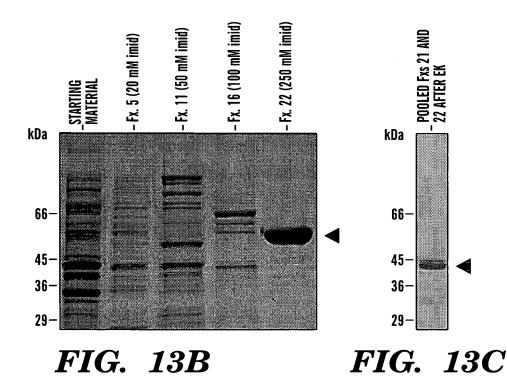


FIG. 13A





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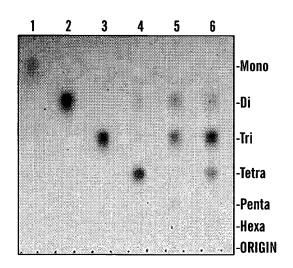


FIG. 14A

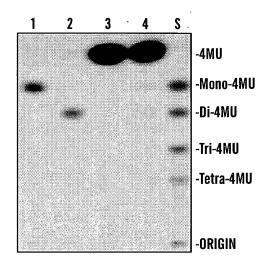


FIG. 14B

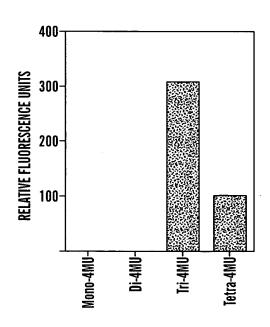


FIG. 14C



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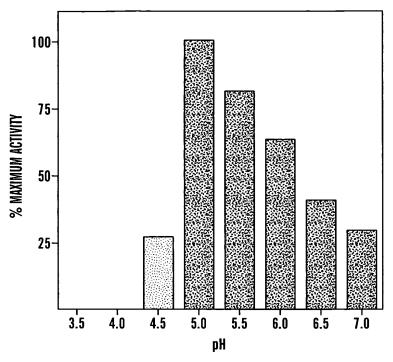


FIG. 15A

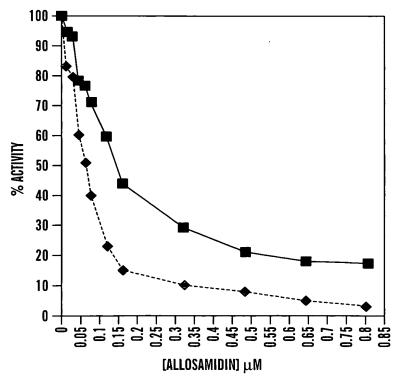


FIG. 15B



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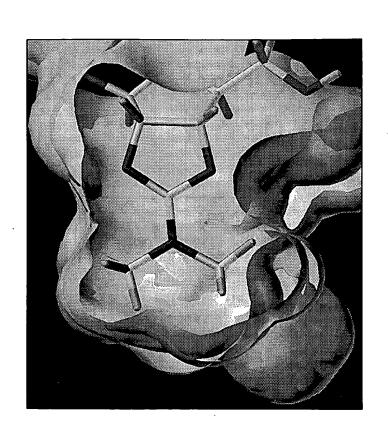


FIG. 16